

SEQUENCE LISTING



<110> Lagarias, John C.

<120> Phytofluors as fluorescent labels

<130> 2500.118US0

<140> 09/272,809

<141> 1998-03-19

<160> 24

<170> PatentIn Ver. 2.0

<210> 1

<211> 748

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Locus SLR0473 =
S6803PHY1 = SYN_PHY

<400> 1

Met Ala Thr Thr Val Gln Leu Ser Asp Gln Ser Leu Arg Gln Leu Glu
1 5 10 15

Thr Leu Ala Ile His Thr Ala His Leu Ile Gln Pro His Gly Leu Val
20 25 30

Val Val Leu Gln Glu Pro Asp Leu Thr Ile Ser Gln Ile Ser Ala Asn
35 40 45

Cys Thr Gly Ile Leu Gly Arg Ser Pro Glu Asp Leu Leu Gly Arg Thr
50 55 60

Leu Gly Glu Val Phe Asp Ser Phe Gln Ile Asp Pro Ile Gln Ser Arg
65 70 75 80

Leu Thr Ala Gly Gln Ile Ser Ser Leu Asn Pro Ser Lys Leu Trp Ala
85 90 95

Arg Val Met Gly Asp Asp Phe Val Ile Phe Asp Gly Val Phe His Arg
100 105 110

Asn Ser Asp Gly Leu Leu Val Cys Glu Leu Glu Pro Ala Tyr Thr Ser
115 120 125

Asp Asn Leu Pro Phe Leu Gly Phe Tyr His Met Ala Asn Ala Ala Leu
130 135 140

Asn Arg Leu Arg Gln Gln Ala Asn Leu Arg Asp Phe Tyr Asp Val Ile
145 150 155 160

Val Glu Glu Val Arg Arg Met Thr Gly Phe Asp Arg Val Met Leu Tyr
165 170 175

Arg Phe Asp Glu Asn Asn His Gly Asp Val Ile Ala Glu Asp Lys Arg
180 185 190

Asp Asp Met Glu Pro Tyr Leu Gly Leu His Tyr Pro Glu Ser Asp Ile
195 200 205

Pro Gln Pro Ala Arg Arg Leu Phe Ile His Asn Pro Ile Arg Val Ile
210 215 220

Pro Asp Val Tyr Gly Val Ala Val Pro Leu Thr Pro Ala Val Asn Pro
225 230 235 240

Ser Thr Asn Arg Ala Val Asp Leu Thr Glu Ser Ile Leu Arg Ser Ala
245 250 255

Tyr His Cys His Leu Thr Tyr Leu Lys Asn Met Gly Val Gly Ala Ser
260 265 270

Leu Thr Ile Ser Leu Ile Lys Asp Gly His Leu Trp Gly Leu Ile Ala
275 280 285

Cys His His Gln Thr Pro Lys Val Ile Pro Phe Glu Leu Arg Lys Ala
290 295 300

Cys Glu Phe Phe Gly Arg Val Val Phe Ser Asn Ile Ser Ala Gln Glu
305 310 315 320

Asp Thr Glu Thr Phe Asp Tyr Arg Val Gln Leu Ala Glu His Glu Ala
325 330 335

Val Leu Leu Asp Lys Met Thr Thr Ala Ala Asp Phe Val Glu Gly Leu
340 345 350

Thr Asn His Pro Asp Arg Leu Leu Gly Leu Thr Gly Ser Gln Gly Ala
355 360 365

Ala Ile Cys Phe Gly Glu Lys Leu Ile Leu Val Gly Glu Thr Pro Asp
370 375 380

Glu Lys Ala Val Gln Tyr Leu Leu Gln Trp Leu Glu Asn Arg Glu Val
385 390 395 400

Gln Asp Val Phe Phe Thr Ser Ser Leu Ser Gln Ile Tyr Pro Asp Ala
405 410 415

Val Asn Phe Lys Ser Val Ala Ser Gly Leu Leu Ala Ile Pro Ile Ala
420 425 430

Arg His Asn Phe Leu Leu Trp Phe Arg Pro Glu Val Leu Gln Thr Val
435 440 445

Asn Trp Gly Gly Asp Pro Asn His Ala Tyr Glu Ala Thr Gln Glu Asp
450 455 460

Gly Lys Ile Glu Leu His Pro Arg Gln Ser Phe Asp Leu Trp Lys Glu
465 470 475 480

Ile Val Arg Leu Gln Ser Leu Pro Trp Gln Ser Val Glu Ile Gln Ser
485 490 495

Ala Leu Ala Leu Lys Lys Ala Ile Val Asn Leu Ile Leu Arg Gln Ala
500 505 510

Glu Glu Leu Ala Gln Leu Ala Arg Asn Leu Glu Arg Ser Asn Ala Asp
515 520 525

Leu Lys Lys Phe Ala Tyr Ile Ala Ser His Asp Leu Gln Glu Pro Leu
530 535 540

Asn Gln Val Ser Asn Tyr Val Gln Leu Leu Glu Met Arg Tyr Ser Glu
545 550 555 560

Ala Leu Asp Glu Asp Ala Lys Asp Phe Ile Asp Phe Ala Val Thr Gly
565 570 575

Val Ser Leu Met Gln Thr Leu Ile Asp Asp Ile Leu Thr Tyr Ala Lys
580 585 590

Val Asp Thr Gln Tyr Ala Gln Leu Thr Phe Thr Asp Val Gln Glu Val
595 600 605

Val Asp Lys Ala Leu Ala Asn Leu Lys Gln Arg Ile Glu Glu Ser Gly
610 615 620

Ala Glu Ile Glu Val Gly Ser Met Pro Ala Val Met Ala Asp Gln Ile
625 630 635 640

Gln Leu Met Gln Val Phe Gln Asn Leu Ile Ala Asn Gly Ile Lys Phe
645 650 655

Ala Gly Asp Lys Ser Pro Lys Ile Lys Ile Trp Gly Asp Arg Gln Glu
660 665 670

Asp Ala Trp Val Phe Ala Val Gln Asp Asn Gly Ile Gly Ile Asp Pro
675 680 685

Gln Phe Phe Glu Arg Ile Phe Val Ile Phe Gln Arg Leu His Thr Arg
690 695 700

Asp Glu Tyr Lys Gly Thr Gly Met Gly Leu Ala Ile Cys Lys Lys Ile
705 710 715 720

Ile Glu Gly His Gln Gly Gln Ile Trp Leu Glu Ser Asn Pro Gly Glu
725 730 735

Gly Ser Thr Phe Tyr Phe Ser Ile Pro Ile Gly Asn
740 745

<210> 2

<211> 1276

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism:cph2 Locus SLL0821

<400> 2

Met Asn Pro Asn Arg Ser Leu Glu Asp Phe Leu Arg Asn Val Ile Asn
1 5 10 15

Lys Phe His Arg Ala Leu Thr Leu Arg Glu Thr Leu Gln Val Ile Val
20 25 30

Glu Glu Ala Arg Ile Phe Leu Gly Val Asp Arg Val Lys Ile Tyr Lys
35 40 45

Phe Ala Ser Asp Gly Ser Gly Glu Val Leu Ala Glu Ala Val Asn Arg
50 55 60

Ala Ala Leu Pro Ser Leu Leu Gly Leu His Phe Pro Val Glu Asp Ile
65 70 75 80

Pro Pro Gln Ala Arg Glu Glu Leu Gly Asn Gln Arg Lys Met Ile Ala

85										90										95																			
Val	Asp	Val	Ala	His	Arg	Arg	Lys	Lys	Ser	His	Glu	Leu	Ser	Gly	Arg																								
100										105										110																			
Ile	Ser	Pro	Thr	Glu	His	Ser	Asn	Gly	His	Tyr	Thr	Thr	Val	Asp	Ser																								
115										120										125																			
Cys	His	Ile	Gln	Tyr	Leu	Leu	Ala	Met	Gly	Val	Leu	Ser	Ser	Leu	Thr																								
130										135										140																			
Val	Pro	Val	Met	Gln	Asp	Gln	Gln	Leu	Trp	Gly	Ile	Met	Ala	Val	His																								
145										150										155										160									
His	Ser	Lys	Pro	Arg	Arg	Phe	Thr	Glu	Gln	Glu	Trp	Glu	Thr	Met	Ala																								
165										170										175																			
Leu	Leu	Ser	Lys	Glu	Val	Ser	Leu	Ala	Ile	Thr	Gln	Ser	Gln	Leu	Ser																								
180										185										190																			
Arg	Gln	Val	His	Gln	Gln	Gln	Val	Gln	Glu	Ala	Leu	Val	Gln	Arg	Leu																								
195										200										205																			
Glu	Thr	Thr	Val	Ala	Gln	Tyr	Gly	Asp	Arg	Pro	Glu	Thr	Trp	Gln	Tyr																								
210										215										220																			
Ala	Leu	Glu	Thr	Val	Gly	Gln	Ala	Val	Glu	Ala	Asp	Gly	Ala	Val	Leu																								
225										230										235										240									
Tyr	Ile	Ala	Pro	Asp	Leu	Thr	Gly	Ser	Val	Ala	Gln	His	Tyr	Gln	Trp																								
245										250										255																			
Asn	Leu	Arg	Phe	Asp	Trp	Gly	Asn	Trp	Leu	Glu	Thr	Ser	Leu	Trp	Gln																								
260										265										270																			
Glu	Leu	Met	Arg	Gly	Gln	Pro	Ser	Ala	Ala	Met	Glu	Pro	Met	Ala	Ala																								
275										280										285																			
Val	Gln	Ser	Thr	Trp	Glu	Lys	Pro	Arg	Pro	Phe	Thr	Ser	Val	Ala	Pro																								
290										295										300																			
Leu	Pro	Pro	Thr	Asn	Cys	Val	Pro	His	Gly	Tyr	Thr	Leu	Gly	Glu	Leu																								
305										310										315										320									
Glu	Gln	Arg	Ser	Asp	Trp	Ile	Ala	Pro	Pro	Glu	Ser	Leu	Ser	Ala	Glu																								
325										330										335																			
Asn	Phe	Gln	Ser	Phe	Leu	Ile	Val	Pro	Leu	Ala	Ala	Asp	Gln	Gln	Trp																								

al
cont.

340 345 350
 Val Gly Ser Leu Ile Leu Leu Arg Lys Glu Lys Ser Leu Val Lys His
 355 360 365
 Trp Ala Gly Lys Arg Gly Ile Asp Arg Arg Asn Ile Leu Pro Arg Leu
 370 375 380
 Ser Phe Glu Ala Trp Glu Glu Thr Gln Lys Leu Val Pro Thr Trp Asn
 385 390 395 400
 Arg Ser Glu Arg Lys Leu Ala Gln Val Ala Ser Thr Gln Leu Tyr Met
 405 410 415
 Ala Ile Thr Gln Gln Phe Val Thr Arg Leu Ile Thr Gln Gln Thr Ala
 420 425 430
 Tyr Asp Pro Leu Thr Gln Leu Pro Asn Trp Ile Ile Phe Asn Arg Gln
 435 440 445
 Leu Thr Leu Ala Leu Leu Asp Ala Leu Tyr Glu Gly Lys Met Val Gly
 450 455 460
 Val Leu Val Ile Ala Met Asp Arg Phe Lys Arg Ile Asn Glu Ser Phe
 465 470 475 480
 Gly His Lys Thr Gly Asp Gly Leu Leu Gln Glu Val Ala Asp Arg Leu
 485 490 495
 Asn Gln Lys Leu Ser Pro Leu Ala Ala Tyr Ser Pro Leu Leu Ser Arg
 500 505 510
 Trp His Gly Asp Gly Phe Thr Ile Leu Leu Thr Gln Ile Ser Asp Asn
 515 520 525
 Gln Glu Met Ile Pro Leu Cys Glu Arg Leu Leu Ser Thr Phe Gln Glu
 530 535 540
 Pro Phe Phe Leu Gln Gly Gln Pro Ile Tyr Leu Thr Ala Ser Met Gly
 545 550 555 560
 Ile Ser Thr Ala Pro Tyr Asp Gly Glu Thr Ala Glu Ser Leu Leu Lys
 565 570 575
 Phe Ala Glu Ile Ala Leu Thr Arg Ala Lys Cys Gln Gly Lys Asn Thr
 580 585 590
 Tyr Gln Phe Tyr Arg Pro Gln Asp Ser Ala Pro Met Leu Asp Arg Leu

595 600 605
 Thr Leu Glu Ser Asp Leu Arg Gln Ala Leu Thr Asn Gln Glu Phe Val
 610 615 620
 Leu Tyr Phe Gln Pro Gln Val Ala Leu Asp Thr Gly Lys Leu Leu Gly
 625 630 635 640
 Val Glu Ala Leu Val Arg Trp Gln His Pro Arg Leu Gly Gln Val Ala
 645 650 655
 Pro Asp Val Phe Ile Pro Leu Ala Glu Glu Leu Gly Leu Ile Asn His
 660 665 670
 Leu Gly Gln Trp Val Leu Glu Thr Ala Cys Ala Thr His Gln His Phe
 675 680 685
 Phe Arg Glu Thr Gly Arg Arg Leu Arg Met Ala Val Asn Ile Ser Ala
 690 695 700
 Arg Gln Phe Gln Asp Glu Lys Trp Leu Asn Ser Val Leu Glu Cys Leu
 705 710 715 720
 Lys Arg Thr Gly Met Pro Pro Glu Asp Leu Glu Leu Glu Ile Thr Glu
 725 730 735
 Ser Leu Met Met Glu Asp Ile Lys Gly Thr Val Val Leu Leu His Arg
 740 745 750
 Leu Arg Glu Glu Gly Val Gln Val Ala Ile Asp Asp Phe Gly Thr Gly
 755 760 765
 Tyr Ser Ser Leu Ser Ile Leu Lys Gln Leu Pro Ile His Arg Leu Lys
 770 775 780
 Ile Asp Lys Ser Phe Val Asn Asp Leu Leu Asn Glu Gly Ala Asp Thr
 785 790 795 800
 Ala Ile Ile Gln Tyr Val Ile Asp Leu Ala Asn Gly Leu Asn Leu Glu
 805 810 815
 Thr Val Ala Glu Gly Ile Glu Ser Glu Ala Gln Leu Gln Arg Leu Gln
 820 825 830
 Lys Met Gly Cys His Leu Gly Gln Gly Tyr Phe Leu Thr Arg Pro Leu
 835 840 845
 Pro Ala Glu Ala Met Met Thr Tyr Leu Tyr Tyr Pro Gln Ile Leu Asp

850 855 860
 Phe Gly Pro Thr Pro Pro Leu Pro Lys Val Ala Leu Pro Glu Thr Glu
 865 870 875 880
 Thr Glu Ala Gly Gln Gly Asn Val Gly Asp Arg Pro Leu Pro Asn Ser
 885 890 895
 Leu Asn Arg Glu Asn Pro Trp Thr Glu Lys Leu His Asp Tyr Val Leu
 900 905 910
 Leu Lys Glu Arg Leu Gln Gln Arg Asn Val Lys Glu Lys Leu Val Leu
 915 920 925
 Lys Ile Ala Asn Lys Ile Arg Ala Ser Leu Asn Ile Asn Asp Ile Leu
 930 935 940
 Tyr Ser Thr Val Thr Glu Val Arg Gln Phe Leu Asn Thr Asp Arg Val
 945 950 955 960
 Val Leu Phe Lys Phe Asn Ser Gln Trp Ser Gly Gln Val Val Thr Glu
 965 970 975
 Ser His Asn Asp Phe Cys Arg Ser Ile Ile Asn Asp Glu Ile Asp Asp
 980 985 990
 Pro Cys Phe Lys Gly His Tyr Leu Arg Leu Tyr Arg Glu Gly Arg Val
 995 1000 1005
 Arg Ala Val Ser Asp Ile Glu Lys Ala Asp Leu Ala Asp Cys His Lys
 1010 1015 1020
 Glu Leu Leu Arg His Tyr Gln Val Lys Ala Asn Leu Val Val Pro Val
 1025 1030 1035 1040
 Val Phe Asn Glu Asn Leu Trp Gly Leu Leu Ile Ala His Glu Cys Lys
 1045 1050 1055
 Thr Pro Arg Tyr Trp Gln Glu Glu Asp Leu Gln Leu Leu Met Glu Leu
 1060 1065 1070
 Ala Thr Gln Val Ala Ile Ala Ile His Gln Gly Glu Leu Tyr Glu Gln
 1075 1080 1085
 Leu Glu Thr Ala Asn Ile Arg Leu Gln Gln Ile Ser Ser Leu Asp Ala
 1090 1095 1100
 Leu Thr Gln Val Gly Asn Arg Tyr Leu Phe Asp Ser Thr Leu Glu Arg

1105 1110 1115 1120
 Glu Trp Gln Arg Leu Gln Arg Ile Arg Glu Pro Leu Ala Leu Leu Leu
 1125 1130 1135
 Cys Asp Val Asp Phe Phe Lys Gly Phe Asn Asp Asn Tyr Gly His Pro
 1140 1145 1150
 Ala Gly Asp Arg Cys Leu Lys Lys Ile Ala Asp Ala Met Ala Lys Val
 1155 1160 1165
 Ala Lys Arg Pro Thr Asp Leu Val Ala Arg Tyr Gly Gly Glu Glu Phe
 1170 1175 1180
 Ala Ile Ile Leu Ser Glu Thr Ser Leu Glu Gly Ala Ile Asn Val Thr
 1185 1190 1195 1200
 Glu Ala Leu Gln Val Glu Val Ala Asn Leu Ala Ile Pro His Thr Val
 1205 1210 1215
 Ser Gly Thr Gly His Val Thr Leu Ser Ile Gly Ile Ala Val Tyr Thr
 1220 1225 1230
 Pro Glu Arg His Ile Asn Pro Asn Ala Leu Val Lys Ala Ala Asp Leu
 1235 1240 1245
 Ala Leu Tyr Glu Ala Lys Ala Lys Gly Arg Asn Gln Trp Leu Ala Tyr
 1250 1255 1260
 Glu Gly Ser Gln Leu Pro His Val Asp Gly Glu Val
 1265 1270 1275

<210> 3
 <211> 481
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:cph Lucus SLL1473
 a 297 aa histidine kinase homolog

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 1 5 10 15
 Met Thr Cys Tyr Leu Trp His Arg Gln Asn Gln Glu Arg Arg Arg Ile
 20 25 30

Glu Ile Ser Ile Lys Gln Gln Thr Gln Arg Glu Arg Phe Ile Asn Gln
35 40 45

Ile Thr Gln His Ile Arg Gln Ser Leu Asn Leu Glu Thr Val Leu Asn
50 55 60

Thr Thr Val Ala Glu Val Lys Thr Leu Leu Gln Val Asp Arg Val Leu
65 70 75 80

Ile Tyr Arg Ile Trp Gln Asp Gly Thr Gly Ser Ala Ile Thr Glu Ser
85 90 95

Val Asn Ala Asn Tyr Pro Ser Ile Leu Gly Arg Thr Phe Ser Asp Glu
100 105 110

Val Phe Pro Val Glu Tyr His Gln Ala Tyr Thr Lys Gly Lys Val Arg
115 120 125

Ala Ile Asn Asp Ile Asp Gln Asp Asp Ile Glu Ile Cys Leu Ala Asp
130 135 140

Phe Val Lys Gln Phe Gly Val Lys Ser Lys Leu Val Val Pro Ile Leu
145 150 155 160

Gln His Asn Arg Ala Ser Ser Leu Asp Asn Glu Ser Glu Phe Pro Tyr
165 170 175

Leu Trp Gly Leu Leu Ile Thr His Gln Cys Ala Phe Thr Arg Pro Trp
180 185 190

Gln Pro Trp Glu Val Glu Leu Met Lys Gln Leu Ala Asn Gln Val Ala
195 200 205

Ile Ala Ile Gln Gln Ser Glu Leu Tyr Glu Gln Leu Gln Gln Leu Asn
210 215 220

Lys Asp Leu Glu Asn Arg Val Glu Lys Arg Thr Gln Gln Leu Ala Ala
225 230 235 240

Thr Asn Gln Ser Leu Arg Met Glu Ile Ser Glu Arg Gln Lys Thr Glu
245 250 255

Ala Ala Leu Arg His Thr Asn His Thr Leu Gln Ser Leu Ile Ala Ala
260 265 270

Ser Pro Arg Gly Ile Phe Thr Leu Asn Leu Ala Asp Gln Ile Gln Ile
275 280 285

Trp Asn Pro Thr Ala Glu Arg Ile Phe Gly Trp Thr Glu Thr Glu Ile
290 295 300

Ile Ala His Pro Glu Leu Leu Thr Ser Asn Ile Leu Leu Glu Asp Tyr
305 310 315 320

Gln Gln Phe Lys Gln Lys Val Leu Ser Gly Met Val Ser Pro Ser Leu
325 330 335

Glu Leu Lys Cys Gln Lys Lys Asp Gly Ser Trp Ile Glu Ile Val Leu
340 345 350

Ser Ala Ala Pro Leu Leu Asp Ser Glu Glu Asn Ile Ala Gly Leu Val
355 360 365

Ala Val Val Ala Asp Ile Thr Glu Gln Lys Arg Gln Ala Glu Gln Ile
370 375 380

Arg Leu Leu Gln Ser Val Val Val Asn Thr Asn Asp Ala Val Val Ile
385 390 395 400

Thr Glu Ala Glu Pro Ile Asp Asp Pro Gly Pro Arg Ile Leu Tyr Val
405 410 415

Asn Glu Ala Phe Thr Lys Ile Thr Gly Tyr Thr Ala Glu Glu Met Leu
420 425 430

Gly Lys Thr Pro Arg Val Leu Gln Gly Pro Lys Thr Ser Arg Thr Glu
435 440 445

Leu Asp Arg Val Arg Gln Ala Ile Ser Gln Trp Gln Ser Val Thr Val
450 455 460

Glu Ala Glu Val Leu Asn Asp Ser Tyr Lys Glu Lys Lys Ser Pro Leu
465 470 475 480

Lys

<210> 4

<211> 1371

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism:cph4 locus SLL1124

(DivJ homolog: PAS domain) a 1372 aa protein that
is more similar to rcaE than to cph1

<400> 4

Met Thr Phe Ala Ala Thr Pro Arg Glu Val Thr Ala Ser Ala Ile Gln
1 5 10 15

Trp Ala Cys Leu Cys Leu Pro Gly Glu Leu Ser Ala Ala Glu Ala Leu
20 25 30

Asn Arg Trp His Arg His Gly Gln Arg Ser Trp Glu Pro Pro Ala Glu
35 40 45

Ala Lys Ala Phe Pro Pro Trp Ala Leu Val Leu Asp Asn Asp Gly Gln
50 55 60

Leu Leu Gly Leu Leu Pro Asp Trp Gln Leu Ala Ala Ala Leu Trp Thr
65 70 75 80

Glu His Phe Ser Pro Ala Ile Ala Leu Ala Glu Leu Cys Leu Pro Cys
85 90 95

Ser Leu Arg Leu Asp Leu Glu Lys Leu Pro Ser Leu Gly Glu Val Met
100 105 110

Gln Ile Phe Ala Thr Trp Gly Tyr Gly Trp Asp Val Ile Pro Val Ala
115 120 125

Asp Arg Gln His Gln Thr Trp Gly Leu Leu Ser Ile Gly Asn Leu Ile
130 135 140

Arg Ser Val Asn Leu Cys Gln Leu Trp Gln Asn Leu Pro Leu Gln Val
145 150 155 160

Thr Ala Ser Pro Pro Leu Cys Leu Gly Thr Glu Thr Thr Leu Gly Glu
165 170 175

Leu Val His His Cys Phe Glu Arg Gln Ile Ser Ser Phe Pro Val Val
180 185 190

Tyr Ser Ser Pro Leu Leu Pro Ala Ala Ala Pro Arg Ile Pro Leu Gly
195 200 205

Asn Val Ser Leu Ser Asn Tyr Phe Lys Gly Pro Asn Tyr Gly Ser Leu
210 215 220

Gly Leu Asp Asn Pro Ile Gly Pro Asp Leu Ser Pro Thr Phe Pro Leu
225 230 235 240

Cys Thr Ile Asn Gln Thr Tyr Cys His Ala Arg Glu Leu Leu Arg Arg
 245 250 255
 Gln Asn Asp Asp Tyr Val Ile Ile Thr Asn Ile Ser Gly Ala Phe Val
 260 265 270
 Gly Trp Val Gly Pro Gln Gln Trp Leu Ala Thr Val Gln Pro Asp Val
 275 280 285
 Leu Leu Glu Ala Leu Gln Arg Glu Val Glu Met Pro Arg Ile Val Gln
 290 295 300
 His Leu Glu Ala Arg Ile Val Trp Gln Gln Gln Gln Gln Arg Asn
 305 310 315 320
 Gln His Leu Ile Gln Lys Leu Leu Ser Arg Asn Pro Asn Leu Ile Tyr
 325 330 335
 Leu Tyr Asp Leu Val Lys Asn Glu Ile Val Tyr Leu Asn Ile Pro Gly
 340 345 350
 Ser Leu Leu Glu Gly Gly Ser Gly Gly Ala Pro Ile Pro Asn Pro Met
 355 360 365
 Val Glu Thr Asp Pro Arg Gln Asp Leu Leu Leu Pro Pro Arg Tyr Phe
 370 375 380
 Gly Leu Glu Glu Leu Ala Ala Leu Gln Ala His Glu Lys Lys Glu Phe
 385 390 395 400
 Asn Phe Glu Phe Thr Asp Gly Gly Gln Ser Val His Tyr Phe Val Val
 405 410 415
 Glu Ile Ser Ala Phe Glu Ile Asp Gly Ser Gly Gln Thr Ser Lys Ile
 420 425 430
 Leu Cys Leu Ala Gln Asp Val Ser His Gly Lys Arg Ala Glu Ala Ala
 435 440 445
 Leu His Thr Lys Glu Gln Gln Leu Gln Thr Leu Val Asn Thr Ile Ala
 450 455 460
 Asp Gly Ile Val Ile Leu Asp Asn His Asp Lys Val Ile Tyr Ala Asn
 465 470 475 480
 Pro Met Ala Cys Gln Met Phe Gly Leu Ser Lys Glu Glu Phe Leu Gln
 485 490 495

a'
 end

Ser Gln Leu Gly Leu Ser Asn Arg Gly Gln Thr Glu Ile Gly Ile Asn
500 505 510

Val Ser Pro Glu Glu Glu Gly Ile Gly Glu Ile Lys Ala Val Pro Ile
515 520 525

His Trp Gln Gly Glu Asp Cys Arg Leu Val Thr Val Arg Asp Val Thr
530 535 540

Asp Arg Gln Arg Val Leu Lys Lys Leu Arg Asp Ser Glu Gln Ile His
545 550 555 560

Arg Ser Leu Leu Glu Ala Leu Pro Asn Leu Val Trp Arg Leu Ser Ser
565 570 575

Ala Gly Asp Val Trp Glu Cys Asn Gln Arg Thr Leu Ala Tyr Phe Gly
580 585 590

Arg Arg Gly Arg Lys Ile Leu Gly Asn Thr Trp Gln Gln Phe Ile Glu
595 600 605

Pro Gly Glu Arg Glu Asn Val Gln Arg Gln Trp Arg Gln Gly Ile Ala
610 615 620

Ala Gln Glu Phe Phe Gln Leu Glu Cys Arg Leu Trp Arg Ser Asp Gly
625 630 635 640

Gln Tyr Arg Trp His Leu Leu Gln Val Leu Pro Leu Glu Asp Arg Phe
645 650 655

Gly Ser Ile Asn Gly Trp Leu Ala Ser Ser Thr Asp Ile Asp Asp Leu
660 665 670

Lys Glu Ala Glu Lys Ala Leu Arg Asn Gln Ala Gln Gln Glu Lys Leu
675 680 685

Leu Ser Ser Ile Ser Gln Arg Ile Arg Glu Ser Leu Lys Leu Glu Thr
690 695 700

Ile Leu Arg Thr Thr Val Thr Glu Val Arg Arg Thr Ile His Ala Asp
705 710 715 720

Arg Val Leu Ile His His Ile Gln Glu Asp Gly Leu Gly Thr Thr Ile
725 730 735

Ala Glu Ser Val Val Asn Gly Gln Pro Ser Val Met Gln Met Asp Leu
740 745 750

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Ser Pro Glu Ser Phe Pro Pro Glu Cys Tyr Gln Arg Tyr Leu Asn Gly
755 760 765

Tyr Ile Tyr Ala Ser Arg Asp Gln Leu Pro Asp Cys Ala Ile Asn Cys
770 775 780

Ala Val Gln Cys Phe Thr Val Ala Glu Ser Gln Ser Arg Ile Val Ala
785 790 795 800

Pro Ile Val Phe Asp His Ser Leu Trp Gly Leu Leu Ile Val His Gln
805 810 815

Cys Ser Ser Ser Arg Thr Trp Gln Thr Ala Glu Ile Gln Leu Met Gln
820 825 830

Ser Leu Gly Asn Gln Leu Ala Ile Ala Ile Gln Gln Ser Leu Leu Tyr
835 840 845

Glu Arg Leu Gln Glu Glu Leu Ser Glu Arg Gln Arg Ala Glu Gln Lys
850 855 860

Leu Leu Glu Val Asn Gln Leu Gln Lys Gly Ile Phe Asp Val Ala Asn
865 870 875 880

Tyr Met Ile Ile Ser Thr Asp Arg Arg Gly Ile Ile Ser Thr Phe Asn
885 890 895

Arg Thr Ala Glu Glu Ile Leu Gly Tyr Thr Ala Ala Glu Leu Ile Gly
900 905 910

Gln Gln Thr Pro Leu Ile Phe His Asp Gln Glu Glu Met Ala Ser Glu
915 920 925

Ala Val Gln Leu Ser Gln Gln Leu Gln Gln Thr Ile Arg Pro Asn Ser
930 935 940

Ile Asp Met Phe Ala Ile Pro Ala Ile Gln Trp Gly Val Tyr Glu Arg
945 950 955 960

Glu Trp Thr Tyr Ile Thr Lys Thr Gly Asp Arg Leu Pro Val Tyr Val
965 970 975

Ser Ile Thr Ala Leu Arg Asp Asp Gln Gly Lys Val Asp Gly Leu Val
980 985 990

Gly Val Ile Thr Asp Leu Arg Arg Gln Lys Gln Ile Glu Arg Glu Arg
995 1000 1005

Gln Asn Leu Asp Phe Val Val Lys Asn Ser Thr Glu Leu Ile Val Ile
 1010 1015 1020
 Thr Asp Leu Glu Gln Lys Val Thr Phe Leu Asn Gln Ala Gly Gln Ser
 1025 1030 1035 1040
 Leu Ile Gly Leu Glu Asn Pro Glu Thr Ala Gln Thr Thr Tyr Leu Ser
 1045 1050 1055
 Glu His Ile Ser Pro Glu Tyr Leu Asn Phe Trp Gln Met Glu Ile Ile
 1060 1065 1070
 Pro Gln Val Phe Arg Ser Gly Ala Trp Glu Gly Glu Phe Ser Leu Gln
 1075 1080 1085
 His Tyr Gln Thr Ala Val Glu Ile Pro Val Thr Ala Ser Val Phe Leu
 1090 1095 1100
 Leu Gln Gly Val Asn Gly Gln His Pro Ala Asn Leu Val Ala Ile Val
 1105 1110 1115 1120
 His Asp Ile Thr His Ile Lys Asn Ala Glu Lys Arg Ile Leu Ala Ala
 1125 1130 1135
 Leu Glu Ala Glu Lys Glu Leu Gly Glu Leu Arg Ser Arg Phe Ile Ser
 1140 1145 1150
 Thr Thr Ser His Glu Phe Arg Thr Pro Leu Ala Ile Ile Ser Ser Ser
 1155 1160 1165
 Thr Gly Ile Leu Lys Lys Tyr Trp Pro Lys Leu Asp Gly Gln Arg Arg
 1170 1175 1180
 Gly Gln His Leu Glu Arg Ile Glu Glu Ser Val His His Met Val Glu
 1185 1190 1195 1200
 Leu Leu Asp Asp Val Leu Thr Ile Asn Arg Ala Glu Thr Lys Tyr Leu
 1205 1210 1215
 Pro Phe Glu Pro Gln Pro Leu Asp Leu Val Ser Phe Cys Arg Gly Ile
 1220 1225 1230
 Thr Asp Glu Leu Gln Ser Ser Thr Glu Tyr His Gly Leu Leu Phe Ser
 1235 1240 1245
 Tyr Asp Gly Leu Gly Pro Gly Glu Ile Val Ala Phe Asp Pro Lys Leu
 1250 1255 1260

Leu Arg Gln Ile Leu Thr Asn Leu Leu Gly Asn Ala Ile Lys Tyr Ser
1265 1270 1275 1280

Pro Ser Gly Gln Pro Val Glu Phe His Leu Gln Arg Arg Gly Asp Val
1285 1290 1295

Gly Ile Phe Ser Val Gln Asp His Gly Ile Gly Ile Gly Pro Glu Asp
1300 1305 1310

Ile Pro Asn Leu Phe Asp Ser Phe Tyr Arg Gly Thr Asn Val Gly Ser
1315 1320 1325

Ile Pro Gly Thr Gly Leu Gly Leu Pro Ile Val Lys Lys Cys Ala Glu
1330 1335 1340

Leu His Gly Gly Met Ile Thr Val Thr Ser Gln Leu Gly Gln Gly Ser
1345 1350 1355 1360

Arg Phe Glu Val Glu Leu Pro Leu Trp Tyr Ser
1365 1370

<210> 5
<211> 891
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown Organism:cph5 locus SLL0041
(locus 1001300) an 891 aa protein,
methyl-accepting chemotaxis protein I. Homology
to tsr in last 250 aa.

<400> 5

Met Ala Glu Ala Phe Ile Ala Glu Asn Thr Ala Val Glu Asp Val Ser
1 5 10 15

Pro Asn Pro Asn Pro Ala Ile Asp Thr Asp Ala Leu Ala Ala Leu Thr
20 25 30

Gln Ser Ala Val Glu Leu Thr Pro Pro Pro Pro Ile Asn Leu Pro Lys
35 40 45

Val Glu Leu Pro Pro Met Gln Pro Leu Ala Pro Leu Met Ala Ile Ala
50 55 60

Asp Pro Asp Asn Leu Ser Pro Met Ser Thr Ser Ile Gln Ala Pro Thr

65											70											75											80
Gln	Ser	Gly	Gly	Leu	Ser	Leu	Arg	Asn	Lys	Ala	Val	Leu	Ile	Ala	Leu																		
				85					90					95																			
Leu	Ile	Gly	Leu	Ile	Pro	Ala	Gly	Val	Ile	Gly	Gly	Leu	Asn	Leu	Ser																		
				100					105					110																			
Ser	Val	Asp	Arg	Leu	Pro	Val	Pro	Gln	Thr	Glu	Gln	Gln	Val	Lys	Asp																		
				115					120					125																			
Ser	Thr	Thr	Lys	Gln	Ile	Arg	Asp	Gln	Ile	Leu	Ile	Gly	Leu	Leu	Val																		
				130					135					140																			
Thr	Ala	Val	Gly	Ala	Ala	Phe	Val	Ala	Tyr	Trp	Met	Val	Gly	Glu	Asn																		
145					150					155					160																		
Thr	Lys	Ala	Gln	Thr	Ala	Leu	Ala	Leu	Lys	Ala	Lys	His	Ser	His	Arg																		
				165					170					175																			
Asn	Leu	Asp	Gln	Pro	Leu	Ala	Val	Ala	Gly	Asp	Glu	Leu	Ala	Ile	Ala																		
				180					185					190																			
Asp	Gln	Thr	Ile	Asp	Ala	Leu	Ser	Ala	Gln	Val	Glu	Lys	Leu	Arg	His																		
				195					200					205																			
Gln	Gln	Asp	Leu	Ser	Leu	Lys	Gln	Ala	Glu	Leu	Leu	Thr	Glu	Leu	Ser																		
				210					215					220																			
Arg	Ala	Asn	Leu	Ser	Asp	Ile	Asp	Glu	Ile	Gln	Gly	Val	Ile	Gln	Lys																		
225					230					235					240																		
Asn	Leu	Asp	Gln	Ala	Arg	Ala	Leu	Phe	Gly	Cys	Glu	Arg	Leu	Val	Phe																		
				245					250					255																			
Tyr	Tyr	His	Pro	Arg	Tyr	Gln	Pro	Glu	Ala	Met	Val	Val	Gln	Ala	Leu																		
				260					265					270																			
Asp	Leu	Thr	Thr	Gln	Gly	Leu	Ile	Asp	Ser	Lys	Asp	Pro	His	Pro	Trp																		
				275					280					285																			
Gly	Gln	Glu	Asp	Met	Pro	Ser	Gln	Ile	Val	Ala	Ile	Asn	Asp	Thr	Ser																		
				290					295					300																			
Gly	Ala	Ser	Ile	Ser	Asn	Pro	His	Arg	Gln	Trp	Leu	Glu	Gln	His	Gln																		
305					310					315					320																		
Val	Lys	Ala	Ser	Leu	Thr	Val	Pro	Leu	His	Arg	Asp	Asn	Tyr	Pro	Leu																		

325	330	335
Gly Leu Leu Met Ala His His Cys Gln Arg Pro His Gln Trp Glu Met		
340	345	350
Arg Glu Arg Gln Phe Leu Gln Gln Leu Thr Glu Glu Leu Gln Thr Thr		
355	360	365
Leu Asp Arg Ala Asn Leu Ile Gln Glu Arg Asn Glu Ser Ala Gln Gln		
370	375	380
Ala Gln Ile Leu Lys Glu Leu Thr Leu Lys Ile Ser Ala Ala Ile Asn		
385	390	395
Ser Glu Gln Val Phe Asp Ile Ala Ala Gln Glu Ile Arg Leu Ala Leu		
405	410	415
Lys Ala Asp Arg Val Ile Val Tyr Arg Phe Asp Ala Thr Trp Ala Gly		
420	425	430
Thr Val Ile Val Glu Ser Val Ala Glu Gly Tyr Pro Lys Ala Leu Gly		
435	440	445
Ala Thr Ile Ala Asp Pro Cys Phe Ala Asp Ser Tyr Val Glu Lys Tyr		
450	455	460
Arg Ser Gly Arg Ile Gln Ala Thr Arg Asp Ile Tyr Asn Ala Gly Leu		
465	470	475
Thr Pro Cys His Ile Gly Gln Leu Lys Pro Phe Glu Val Lys Ala Asn		
485	490	495
Leu Val Ala Pro Ile Asn Tyr Lys Gly Asn Leu Leu Gly Leu Leu Ile		
500	505	510
Ala His Gln Cys Ser Gly Pro Arg Asp Trp His Gln Asn Glu Ile Asp		
515	520	525
Leu Phe Gly Gln Leu Thr Val Gln Val Gly Leu Ala Leu Glu Arg Ser		
530	535	540
Asp Leu Leu Ala Gln Gln Lys Ile Ala Glu Val Glu Gln Arg Gln Met		
545	550	555
Arg Glu Lys Met Gln Lys Arg Ala Leu Glu Leu Leu Met Glu Val Asp		
565	570	575
Pro Val Ser Arg Gly Asp Leu Thr Ile Arg Ala His Val Thr Glu Asp		

at
cont.

580 585 590
 Glu Ile Gly Thr Ile Ala Asp Ser Tyr Asn Ala Thr Ile Glu Ser Leu
 595 600 605
 Arg Arg Ile Val Thr Gln Val Gln Thr Ala Ala Ser Gln Phe Thr Glu
 610 615 620
 Thr Thr Asp Thr Asn Glu Val Ala Val Arg Gln Leu Ala Gln Gln Ala
 625 630 635 640
 Asn Arg Gln Ala Leu Asp Val Ala Glu Ala Leu Glu Arg Leu Gln Ala
 645 650 655
 Met Asn Lys Ser Ile Gln Ala Val Ala Glu Asn Ala Ala Gln Ala Glu
 660 665 670
 Ser Ala Val Gln Arg Ala Thr Gln Thr Val Asp Gln Gly Glu Asp Ala
 675 680 685
 Met Asn Arg Thr Val Asp Gly Ile Val Ala Ile Arg Glu Thr Val Ala
 690 695 700
 Ala Thr Ala Lys Gln Val Lys Arg Leu Gly Glu Ser Ser Gln Lys Ile
 705 710 715 720
 Ser Lys Val Val Asn Leu Ile Gly Ser Phe Ala Asp Gln Thr Asn Leu
 725 730 735
 Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala His Ala Gly Glu Glu Gly
 740 745 750
 Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg Ser Leu Ala Arg Gln
 755 760 765
 Ser Ala Glu Ala Thr Ala Glu Ile Ala Gln Leu Val Ala Thr Ile Gln
 770 775 780
 Ala Glu Thr Asn Glu Val Val Asn Ala Met Glu Ala Gly Thr Glu Gln
 785 790 795 800
 Val Val Val Gly Thr Lys Leu Val Glu Glu Thr Arg Arg Ser Leu Asn
 805 810 815
 Gln Ile Thr Ala Val Ser Ala Gln Ile Ser Gly Leu Val Glu Ala Ile
 820 825 830
 Thr Ser Ala Ala Ile Glu Gln Ser Gln Thr Ser Glu Ser Val Thr Gln

a'
 cont.

835 840 845

Thr Met Ala Leu Val Ala Gln Ile Ala Asp Lys Asn Ser Ser Glu Ala
850 855 860

Ser Gly Val Ser Ala Thr Phe Lys Glu Leu Leu Ala Val Ala Gln Ser
865 870 875 880

Leu Gln Glu Ala Val Lys Gln Phe Lys Val Gln
885 890

<210> 6
<211> 844
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:cph6 locus
SLR12112 (ETR1 homolog; PAS domain) an 844 aa
protein. Chromophore domain 461-628.

<400> 6

Met Ala Ile Thr Ala Phe Thr Leu Gly Asp Phe Phe Gln Ala Asn Ser
1 5 10 15

Tyr Ile Pro His Gly His Cys Tyr Leu Trp Gln Thr Pro Leu Val Trp
20 25 30

Leu His Val Ser Ala Asp Phe Phe Thr Ala Ile Ala Tyr Tyr Ser Ile
35 40 45

Pro Leu Thr Leu Leu Tyr Phe Leu Arg Lys Arg Gln Asp Ile Pro Phe
50 55 60

Pro Asn Ile Ile Phe Leu Phe Ser Thr Phe Ile Leu Cys Cys Gly Thr
65 70 75 80

Ser His Phe Phe Asp Ile Ile Thr Leu Trp Tyr Pro Ile Tyr Trp Ile
85 90 95

Ser Gly Thr Val Lys Ala Ser Met Ala Ile Val Ser Ile Ile Thr Val
100 105 110

Phe Glu Leu Ile Gln Ile Val Pro Asn Ala Leu Asn Leu Lys Ser Pro
115 120 125

Thr Glu Leu Ala Thr Leu Asn Leu Ala Leu Asn Gln Glu Ile Lys Glu

130 135 140
 Arg Gln Thr Ala Glu Ile Ala Leu Gln Glu Leu Asn Asn Asn Leu Glu
 145 150 155 160
 Lys Arg Val Glu Asp Arg Thr Thr Gln Leu Ala Lys Ile Asn Gln Gln
 165 170 175
 Leu Glu Gln Glu Ile Glu Asp Lys Thr Arg Ala Lys Glu Asp Leu Glu
 180 185 190
 Lys Asn Lys Asp Gln Leu Ala Gln Leu Ala Ala Ile Val Glu Ser Ser
 195 200 205
 Gln Asp Ala Ile Ile Ser Lys Thr Leu Asp Gly Asn Ile Thr Ser Trp
 210 215 220
 Asn Glu Ser Ala Glu Arg Leu Phe Gly Tyr Thr Ala Glu Glu Met Ile
 225 230 235 240
 Gly Ser His Ile Thr Lys Leu Ile Pro Glu Glu Leu Ile Leu Glu Glu
 245 250 255
 Asp Leu Ile Ala Glu Cys Ile Arg Gln Gly Gln Arg Ile Asn Thr Tyr
 260 265 270
 Glu Thr Gln Arg Gln Arg Lys Asp Gly Thr Lys Ile Asp Val Ala Leu
 275 280 285
 Thr Ile Ser Pro Ile Arg Asp Glu His Lys Asn Val Val Gly Ala Ser
 290 295 300
 Lys Ile Val Arg Asp Ile Thr Ala Arg Leu Asp Val Glu Asn Ala Leu
 305 310 315 320
 Arg Glu Ser Gln Tyr Phe Ile Glu Lys Leu Ala Asn Tyr Ser Pro Gln
 325 330 335
 Ile Leu Tyr Ile Leu Asp Pro Ile Ala Trp Lys Asn Ile Tyr Val Asn
 340 345 350
 Tyr Gln Ser Phe Glu Ile Leu Gly Tyr Thr Pro Glu Glu Phe Lys Asn
 355 360 365
 Gly Gly Thr Glu Leu Leu Leu Asn Ile Val His Pro Asp Asp Ile Pro
 370 375 380
 Thr Leu Tyr Glu Asn Lys Asn Phe Trp Gln Lys Ser Gln Glu Gly Gln

a'
 cont.

385 390 395 400
 Val Leu Thr Thr Glu Tyr Arg Met Arg His Lys Asn Gly Ser Trp Arg
 405 410 415
 Trp Leu Arg Ser Arg Glu Val Val Phe Ala Arg Asp Asp Tyr Gly Gln
 420 425 430
 Val Thr Lys Val Leu Gly Thr Ala Gln Asp Ile Ser Asp Ser Lys Glu
 435 440 445
 Gln Glu Gln Arg Leu Tyr Glu Gln Gly Arg Arg Glu Ser Leu Leu Arg
 450 455 460
 Glu Ile Thr Gln Arg Ile Arg Gln Ser Leu Asp Leu Pro Thr Ile Phe
 465 470 475 480
 Asn Thr Val Val Gln Glu Ile Arg Gln Phe Leu Glu Ala Asp Arg Val
 485 490 495
 Val Ile Phe Gln Phe Ser Pro Asp Ser Asp Phe Ser Val Gly Asn Ile
 500 505 510
 Val Ala Glu Ser Val Leu Ala Pro Phe Lys Pro Ile Ile Asn Ser Ala
 515 520 525
 Ile Glu Glu Thr Cys Phe Ser Asn Asn Tyr Ala Gln Arg Tyr Gln Gln
 530 535 540
 Gly Arg Ile Gln Val Ile Glu Asp Ile His Gln Ser His Leu Arg Gln
 545 550 555 560
 Cys His Ile Asp Phe Leu Ala Arg Leu Gln Val Arg Ala Asn Leu Val
 565 570 575
 Leu Pro Leu Ile Asn Asp Ala Ile Leu Trp Gly Leu Leu Cys Ile His
 580 585 590
 Gln Cys Asp Ser Ser Arg Val Trp Glu Gln Thr Glu Ile Asp Leu Leu
 595 600 605
 Lys Gln Ile Thr Asn Gln Phe Glu Ile Ala Ile Gln Gln Ala Thr Leu
 610 615 620
 Tyr Glu Gln Ala Gln Gln Glu Leu Ala Ser Lys Asn Gln Leu Phe Val
 625 630 635 640
 Gln Leu Thr Asn Glu Leu Glu Gln Lys Lys Val Leu Leu Lys Glu Ile

a'
 int.

645	650	655
His His Arg Val Lys Asn Asn Leu Gln Ile Met Ser Ser Leu Leu Tyr		
660	665	670
Leu Gln Phe Ser Lys Ala Ser Pro Ala Ile Gln Gln Leu Ser Glu Glu		
675	680	685
Tyr Gln Asn Arg Ile Gln Ser Met Ala Leu Ile His Glu Gln Leu Tyr		
690	695	700
Arg Ser Glu Asp Leu Ala Asn Ile Asp Phe Ser Gln Tyr Leu Lys Asn		
705	710	715 720
Leu Thr His Asn Ile Cys Gln Ser Tyr Gly Cys Asn Thr Asp Ser Ile		
725	730	735
Lys Ile Lys Leu Leu Val Glu Gln Val Lys Val Pro Leu Glu Gln Ser		
740	745	750
Ile Pro Leu Gly Leu Ile Ile Gln Glu Leu Val Ser Asn Ala Leu Lys		
755	760	765
His Ala Phe Pro Thr Thr Glu Gly Glu Ile Ser Ile Lys Phe Thr Ser		
770	775	780
Met Asn Ser His Tyr Ser Leu Gln Val Trp Asp Asn Gly Val Gly Ile		
785	790	795 800
Ser Arg Asp Ile Asp Leu Glu Asn Thr Asp Ser Leu Gly Met Gln Leu		
805	810	815
Ile Tyr Ser Leu Thr Glu Gln Leu Gln Gly Glu Leu His Tyr Glu Tyr		
820	825	830
Val Gly Gly Ala Gln Phe Gly Leu Glu Phe Ser Leu		
835	840	

<210> 7
 <211> 950
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:coh7 (locus SLR
 1393) a 950 aa protein. Chromophore domain
 402-620. Contains a histidine kinase transmitter

domain.

<400> 7

Met Ser Pro Ser Ser His Gly Thr Ala Val Gln Gln Ala Ile Ala Asp
1 5 10 15

Gln Leu Leu Glu Met Ile Leu Gln Ser Gln Asp Leu His Asn Ala Tyr
20 25 30

Arg Leu Val Val Glu Gly Leu Gln Arg Gly Leu Gly Val Asp Arg Val
35 40 45

Leu Leu Val Gln Asn Ala Val Phe Pro Asn Arg Gln Ser Arg Leu Val
50 55 60

Ala Gln Ala Ile Ala Pro Ala Arg Asp Ile Met Leu Leu Asp Glu Pro
65 70 75 80

Cys Ala Asp Cys Arg Trp Leu His Leu Leu Gly Gln Leu Pro His Tyr
85 90 95

Gly Leu Trp Thr Val Trp Glu Gly Glu Gly Glu Phe Val Gln Leu Asp
100 105 110

Pro Val Gln Gly Glu Phe Cys Arg Thr Leu Gly Ile Lys Ser Leu Leu
115 120 125

His Leu Pro Leu Val Ile Asn Gln Arg His Trp Gly Val Leu Ser Leu
130 135 140

Gln Tyr Leu His Gln Ala Arg Pro Trp Pro Leu Glu Asp Gln Gln Phe
145 150 155 160

Ala Gln Arg Ile Ala His Leu Phe Cys Leu Gly Leu Met Lys Thr Glu
165 170 175

Leu Trp Ile His Cys Gln Asn His Lys Asn Ala Leu Gln Thr Val Val
180 185 190

Ala Glu Gly Gln Val Gln Arg Glu Thr Tyr Leu Lys Ser Ala Gln Arg
195 200 205

Glu Arg Ala Ile Ala Asp Val Ile Asp Lys Ile Arg Phe Ala Leu Asp
210 215 220

Leu Arg Ser Leu Phe Gln Thr Thr Val Thr Glu Val Arg Lys Leu Leu
225 230 235 240

Val Ala Asp Arg Val Met Ile Ile Lys Val Arg Gln Asn Lys Asn Phe
 245 250 255
 Ser Trp Gly Glu Ile Gln Ala Glu Ala Gln Thr Asp Asp Lys Leu Cys
 260 265 270
 Leu Leu Pro Pro Lys Glu Arg Val Pro Leu Ser Ser Arg Trp Ile Asp
 275 280 285
 His Phe Ala Lys Gly Leu Ile Leu Ala Met Asp Asp Thr Asp Asp Gln
 290 295 300
 Arg Ala Asp Phe Asp Gln Ser Met Leu Ala Leu Ala Lys Ala Asn Leu
 305 310 315 320
 Val Val Pro Leu Phe Ser Gly Asp Arg Leu Trp Gly Val Leu Ser Val
 325 330 335
 His Gln Cys Asp Gly Pro Arg Val Trp Glu Ser Ser Asp Ile Glu Phe
 340 345 350
 Ala Leu Lys Ile Ala Leu Asn Leu Gly Val Ala Leu Gln Gln Ala Glu
 355 360 365
 Leu Leu Thr Glu Ser Gln Arg Arg Ser Thr Ala Leu Gln Ser Ala Leu
 370 375 380
 Gly Glu Val Glu Ala Gln Lys Asp Tyr Leu Ala Arg Ile Ala Glu Glu
 385 390 395 400
 Glu Arg Ala Leu Thr Arg Val Ile Glu Gly Ile Arg Gln Thr Leu Glu
 405 410 415
 Leu Gln Asn Ile Phe Arg Ala Thr Ser Asp Glu Val Arg His Leu Leu
 420 425 430
 Ser Cys Asp Arg Val Leu Val Tyr Arg Phe Asn Pro Asp Trp Ser Gly
 435 440 445
 Glu Phe Ile His Glu Ser Val Ala Gln Met Trp Glu Pro Leu Lys Asp
 450 455 460
 Leu Gln Asn Asn Phe Pro Leu Trp Gln Asp Thr Tyr Leu Gln Glu Asn
 465 470 475 480
 Glu Gly Gly Arg Tyr Arg Asn His Glu Ser Leu Ala Val Gly Asp Val
 485 490 495

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 cont.

Glu Thr Ala Gly Phe Thr Asp Cys His Leu Asp Asn Leu Arg Arg Phe
500 505 510

Glu Ile Arg Ala Phe Leu Thr Val Pro Val Phe Val Gly Glu Gln Leu
515 520 525

Trp Gly Leu Leu Gly Ala Tyr Gln Asn Gly Ala Pro Arg His Trp Gln
530 535 540

Ala Arg Glu Ile His Leu Leu His Gln Ile Ala Asn Gln Leu Gly Val
545 550 555 560

Ala Val Tyr Gln Ala Gln Leu Leu Ala Arg Phe Gln Glu Gln Ser Lys
565 570 575

Thr Met Glu Asn Thr Leu Ala Asp Leu Thr Ala Ile Val Asp Asn Leu
580 585 590

Ala Asp Gly Leu Leu Val Ile Asp Leu Phe Gly Arg Ile Thr Arg Tyr
595 600 605

Asn Pro Ala Leu Leu Ala Met Phe Asp Leu Glu Gly Leu Glu Leu Leu
610 615 620

Gly Ala Gly Val Asp Ala Tyr Phe Pro Glu Thr Leu Asn Gln Leu Leu
625 630 635 640

Ala Lys Pro Glu Arg Glu Glu Gln Lys Leu Val Thr Ala Asp Val Glu
645 650 655

Leu Ser Gln Gly Arg Gln Gly Gln Ala Leu Ile Thr Ser Ile Thr Ser
660 665 670

His Glu Asn Gly Cys Glu Tyr Pro Gln Cys Leu Gly Ala Val Ile Met
675 680 685

Ile Arg Asp Val Thr His Glu Arg Glu Val Glu Arg Met Lys Thr Asp
690 695 700

Phe Leu Ala Thr Val Ser His Glu Leu Arg Thr Pro Leu Thr Ser Ile
705 710 715 720

Leu Gly Phe Ala Thr Val Ile Gln Asp Lys Leu Asn Arg Val Ile Ile
725 730 735

Pro Glu Leu Asp Leu Ala Gln Pro His Leu Gly Lys Ala Thr Glu Arg
740 745 750

Val Met Arg Asn Leu Ala Ile Ile Glu Ser Glu Ala Gln Arg Leu Thr
755 760 765

Val Leu Ile Asn Asp Val Leu Asp Ile Ala Lys Met Glu Ala Gly Gln
770 775 780

Glu Ser Trp Gln Glu Gln Pro Cys Ala Ile Gly Pro Ile Ile Glu Arg
785 790 795 800

Ala Ile Ala Thr Ile Thr Pro Gln Ala Gln Lys Lys Asn Ile Ser Leu
805 810 815

Gln Gly Asp Leu Glu Pro Gly Leu Pro Asp Phe Ile Gly Asp Glu Asn
820 825 830

Arg Ile Leu Gln Val Val Leu Asn Leu Leu Ser Asn Ala Val Lys Phe
835 840 845

Thr Pro Lys Gly Leu Ile Thr Ala Arg Ser His Phe His Gln Asn Tyr
850 855 860

Leu Trp Val Glu Ile Ile Asp His Gly Pro Gly Ile His Pro Ala Asp
865 870 875 880

Gln Glu Lys Ile Phe Glu Pro Phe Gln Gln Gly Gly Gly Asp Val Leu
885 890 895

Thr Asp Lys Pro Gln Gly Thr Gly Leu Gly Leu Pro Ile Cys Lys Lys
900 905 910

Ile Val Glu His His Gly Gly Thr Ile Gly Val Asn Ser Ser Leu Gly
915 920 925

Arg Gly Ser Thr Phe Tyr Phe Ser Leu Pro Val Pro Val Pro Ala Val
930 935 940

Glu Thr Ser Pro Ala Val
945 950

<210> 8
<211> 750
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:cph8 (locus
SLR1969) A 750 aa protein. Chromophore domain

156-347. Contains a histidine kinase transmitter domain.

<400> 8

Met Leu Pro Ala Phe Ser Pro Ile Phe Arg Arg Leu Leu Pro Ala Val
1 5 10 15

Thr Phe Glu Arg Leu Leu Arg Phe Trp Arg Thr Leu Ala Gln Gln Thr
20 25 30

Gly Asp Gly Val Gln Cys Phe Val Gly Asp Leu Pro Ser Ser Leu Lys
35 40 45

Pro Pro Pro Gly Pro Ser Val Leu Glu Ala Glu Val Asp His Arg Phe
50 55 60

Ala Leu Leu Val Ser Pro Gly Gln Trp Ala Leu Leu Glu Gly Glu Gln
65 70 75 80

Ile Ser Pro His His Tyr Ala Val Ser Ile Thr Phe Ala Gln Gly Ile
85 90 95

Ile Glu Asp Phe Ile Gln Lys Gln Asn Leu Pro Val Val Ala Glu Ala
100 105 110

Met Pro His Arg Pro Glu Thr Pro Ser Gly Pro Thr Ile Ala Glu Gln
115 120 125

Leu Thr Leu Gly Leu Leu Glu Ile Leu Asn Ser Asp Ser Thr Ser Phe
130 135 140

Ser Pro Glu Pro Ser Leu Gln Asp Ser Leu Gln Ala Ser Gln Val Lys
145 150 155 160

Leu Leu Ser Gln Val Ile Ala Gln Ile Arg Gln Ser Leu Asp Leu Ser
165 170 175

Glu Ile Leu Asn Asn Ala Val Thr Ala Val Gln Lys Phe Leu Phe Val
180 185 190

Asp Arg Leu Val Ile Tyr Gln Phe His Tyr Ser Gln Pro Ser Leu Thr
195 200 205

Pro Leu Glu Glu Asn Gln Ile Pro Ala Pro Arg Pro Arg Gln Gln Tyr
210 215 220

Gly Glu Val Thr Tyr Glu Ala Arg Arg Ser Pro Glu Ile Asp Thr Met
225 230 235 240

Leu Gly Ile Met Thr Glu Asn Asp Cys Phe Ser Gln Val Phe Ser Tyr
 245 250 255

Glu Gln Lys Tyr Leu Lys Gly Ala Val Val Ala Val Ser Asp Ile Glu
 260 265 270

Asn His Tyr Ser Ser Ser Tyr Cys Leu Val Gly Leu Leu Gln Arg Tyr
 275 280 285

Gln Val Arg Ala Lys Leu Val Ala Pro Ile Ile Val Glu Gly Gln Leu
 290 295 300

Trp Gly Leu Leu Ile Ala His Gln Cys His His Pro Arg Gln Trp Leu
 305 310 315 320

Asp Ser Glu Lys Asn Phe Leu Gly Gln Ile Gly Glu His Leu Ala Val
 325 330 335

Ala Ile Val Gln Ser Leu Leu Tyr Ser Glu Val Gln Lys Gln Lys Asn
 340 345 350

Asn Phe Glu Lys Arg Val Ile Glu Arg Thr Lys Glu Leu Arg Asp Thr
 355 360 365

Leu Met Ala Ala Gln Ala Ala Asn Leu Leu Lys Ser Gln Phe Ile Asn
 370 375 380

Asn Ile Ser His Glu Leu Arg Thr Pro Leu Thr Ser Ile Ile Gly Leu
 385 390 395 400

Ser Ala Thr Leu Leu Arg Trp Phe Asp His Pro Ala Ser Leu Pro Pro
 405 410 415

Ala Lys Gln Gln Tyr Tyr Leu Leu Asn Ile Gln Glu Asn Gly Lys Lys
 420 425 430

Leu Leu Asp Gln Ile Asn Ser Ile Ile Gln Leu Ser Gln Leu Glu Ser
 435 440 445

Gly Gln Thr Ala Leu Asn Cys Gln Ser Phe Ser Leu His Thr Leu Ala
 450 455 460

Gln Thr Val Ile His Ser Leu Leu Gly Val Ala Ile Lys Gln Gln Ile
 465 470 475 480

Asn Leu Glu Leu Asp Tyr Gln Ile Asn Val Gly Gln Asp Gln Phe Cys
 485 490 495

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Ala Asp Gln Glu Arg Leu Asp Gln Ile Leu Thr Gln Leu Leu Asn Asn
 500 505 510

Ala Leu Lys Phe Thr Pro Ala Glu Gly Thr Val Ile Leu Arg Ile Trp
 515 520 525

Lys Glu Ser Asn Gln Ala Ile Phe Gln Val Glu Asp Thr Gly Ile Gly
 530 535 540

Ile Asn Glu Gln Gln Leu Pro Val Leu Phe Glu Ala Phe Lys Val Ala
 545 550 555 560

Gly Asp Ser Tyr Thr Ser Phe Tyr Glu Thr Gly Gly Val Gly Leu Ala
 565 570 575

Leu Thr Lys Gln Leu Val Glu Leu His Gly Gly Tyr Ile Glu Val Glu
 580 585 590

Ser Ser Pro Gly Gln Gly Thr Ile Phe Thr Thr Val Ile Pro Gln Gln
 595 600 605

Asn Phe Pro Pro Thr Thr Lys Gly Gln Val Gln Asp Lys Leu Asp Ala
 610 615 620

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Ala Met Pro Phe Asn Ser Ser Val Ile Val Ile Glu Gln Asp Glu Glu
 625 630 635 640

Ile Ala Thr Leu Ile Cys Glu Leu Leu Thr Val Ala Asn Tyr Gln Val
 645 650 655

Ile Trp Leu Ile Asp Thr Thr Asn Ala Leu Gln Gln Val Glu Leu Leu
 660 665 670

Gln Pro Gly Leu Ile Ile Val Asp Gly Asp Phe Val Asp Val Thr Glu
 675 680 685

Val Thr Arg Gly Ile Lys Lys Ser Arg Arg Ile Ser Lys Val Thr Val
 690 695 700

Phe Leu Leu Ser Glu Ser Leu Ser Ser Ala Glu Trp Gln Ala Leu Ser
 705 710 715 720

Gln Lys Gly Ile Asp Asp Tyr Leu Leu Lys Pro Leu Gln Pro Glu Leu
 725 730 735

Leu Leu Gln Arg Val Gln Ser Ile Gln Gln Glu Pro Leu Arg
 740 745 750

<210> 9
<211> 196
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:Atphye

<400> 9
Lys Leu Ala Val Arg Ala Ile Ser Arg Leu Gln Ser Leu Pro Gly Gly
1 5 10 15

Asp Ile Gly Ala Leu Cys Asp Thr Val Val Glu Asp Val Gln Arg Leu
20 25 30

Thr Gly Tyr Asp Arg Val Met Val Tyr Gln Phe His Glu Asp Asp His
35 40 45

Gly Glu Val Val Ser Glu Ile Arg Arg Ser Asp Leu Glu Pro Tyr Leu
50 55 60

Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ala Arg Phe Leu
65 70 75 80

Phe Lys Gln Asn Arg Val Arg Met Ile Cys Asp Cys Asn Ala Thr Pro
85 90 95

Val Lys Val Val Gln Ser Glu Glu Leu Lys Arg Pro Leu Cys Leu Val
100 105 110

Asn Ser Thr Leu Arg Ala Pro His Gly Cys His Thr Gln Tyr Met Ala
115 120 125

Asn Met Gly Ser Val Ala Ser Leu Ala Leu Ala Ile Val Val Lys Gly
130 135 140

Lys Asp Ser Ser Lys Leu Trp Gly Leu Val Val Gly His His Cys Ser
145 150 155 160

Pro Arg Tyr Val Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met
165 170 175

Gln Ala Phe Gly Leu Gln Leu Gln Met Glu Leu Gln Leu Ala Ser Gln
180 185 190

Leu Ala Glu Lys

<210> 10
 <211> 207
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:Atphyb

<400> 10
 Lys Leu Ala Val Arg Ala Ile Ser Gln Leu Gln Ala Leu Pro Gly Gly
 1 5 10 15
 Asp Ile Lys Leu Leu Cys Asp Thr Val Val Glu Ser Val Arg Asp Leu
 20 25 30
 Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp Glu His
 35 40 45
 Gly Glu Val Val Ala Glu Ser Lys Arg Asp Asp Leu Glu Pro Tyr Ile
 50 55 60
 Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg Phe Leu
 65 70 75 80
 Phe Lys Gln Asn Arg Val Arg Met Ile Val Asp Cys Asn Ala Thr Pro
 85 90 95
 Val Leu Val Val Gln Asp Asp Arg Leu Thr Gln Ser Met Cys Leu Val
 100 105 110
 Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ser Gln Tyr Met Ala
 115 120 125
 Asn Met Gly Ser Ile Ala Ser Leu Ala Met Ala Val Ile Ile Asn Gly
 130 135 140
 Asn Glu Asp Asp Gly Ser Asn Val Ala Ser Gly Arg Ser Ser Met Arg
 145 150 155 160
 Leu Trp Gly Leu Val Val Cys His His Thr Ser Ser Arg Cys Ile Pro
 165 170 175
 Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu
 180 185 190

Gln Leu Asn Met Glu Leu Gln Leu Ala Leu Gln Met Ser Glu Lys
 195 200 205

<210> 11
 <211> 210
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:Mcphylb

<400> 11
 Lys Leu Ala Ala Lys Ala Ile Ser Arg Leu Gln Ser Leu Pro Gly Gly
 1 5 10 15

Asp Ile Gly Leu Leu Cys Asp Ala Val Val Glu Glu Val Arg Glu Leu
 20 25 30

Thr Gly Tyr Asp Arg Val Met Ala Tyr Lys Phe His Glu Asp Glu His
 35 40 45

Gly Glu Val Ile Ala Glu Ile Arg Arg Ser Asp Leu Glu Pro Tyr Leu
 50 55 60

Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ala Arg Phe Leu
 65 70 75 80

Phe Met Lys Asn Arg Val Arg Ile Ile Cys Asp Cys Ser Ala Pro Pro
 85 90 95

Val Lys Val Ile Gln Asp Pro Thr Met Lys His Pro Ile Ser Leu Ala
 100 105 110

Gly Ser Thr Leu Arg Gly Val His Gly Cys His Ala Gln Tyr Met Ala
 115 120 125

Asn Met Gly Ser Val Ala Ser Leu Val Met Ala Val Ile Ile Asn Asp
 130 135 140

Asn Ser Ser Glu Glu Gly Ala Thr Ala Ala Gly Gly Ile Leu His Lys
 145 150 155 160

Gly Arg Lys Leu Trp Gly Leu Val Val Cys His His Ser Ser Pro Arg
 165 170 175

Tyr Val Pro Phe Pro Leu Arg Ser Ala Cys Glu Phe Leu Met Gln Val
 180 185 190

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Phe Gly Leu Gln Leu Asn Met Glu Val Glu Leu Ser Ser Gln Leu Arg
 195 200 205

Glu Lys
 210

<210> 12
 <211> 206
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:Atphyc

<400> 12
 Lys Leu Ala Ala Lys Ser Ile Ser Arg Leu Gln Ala Leu Pro Ser Gly
 1 5 10 15

Asn Met Leu Leu Leu Cys Asp Ala Leu Val Lys Glu Val Ser Glu Leu
 20 25 30

Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp Gly His
 35 40 45

Gly Glu Val Ile Ala Glu Cys Cys Arg Glu Asp Met Glu Pro Tyr Leu
 50 55 60

Gly Leu His Tyr Ser Ala Thr Asp Ile Pro Gln Ala Ser Arg Phe Leu
 65 70 75 80

Phe Met Arg Asn Lys Val Arg Met Ile Cys Asp Cys Ser Ala Val Pro
 85 90 95

Val Lys Val Val Gln Asp Lys Ser Leu Ser Gln Pro Ile Ser Leu Ser
 100 105 110

Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr Met Ser
 115 120 125

Asn Met Gly Ser Val Ala Ser Leu Val Met Ser Val Thr Ile Asn Gly
 130 135 140

Ser Asp Ser Asp Glu Met Asn Arg Asp Leu Gln Thr Gly Arg His Leu
 145 150 155 160

Trp Gly Leu Val Val Cys His His Ala Ser Pro Arg Phe Val Pro Phe

165 170 175
 Pro Leu Arg Tyr Ala Cys Glu Phe Leu Thr Gln Val Phe Gly Val Gln
 180 185 190

 Ile Asn Lys Glu Ala Glu Ser Ala Val Leu Leu Lys Glu Lys
 195 200 205

 <210> 13
 <211> 210
 <212> PRT
 <213> Unknown

 <220>
 <223> Description of Unknown Organism: Atphyra

 <400> 13
 Lys Leu Ala Ala Lys Ala Ile Thr Arg Leu Gln Ser Leu Pro Ser Gly
 1 5 10 15

 Ser Met Glu Arg Leu Cys Asp Thr Met Val Gln Glu Val Phe Glu Leu
 20 25 30

 Thr Gly Tyr Asp Arg Val Met Ala Tyr Lys Phe His Glu Asp Asp His
 35 40 45

 Gly Glu Val Val Ser Glu Val Thr Lys Pro Gly Leu Glu Pro Tyr Leu
 50 55 60

 Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ala Arg Phe Leu
 65 70 75 80

 Phe Met Lys Asn Lys Val Arg Met Ile Val Asp Cys Asn Ala Lys His
 85 90 95

 Ala Arg Val Leu Gln Asp Glu Lys Leu Ser Phe Asp Leu Thr Leu Cys
 100 105 110

 Gly Ser Thr Leu Arg Ala Pro His Ser Cys His Leu Gln Tyr Met Ala
 115 120 125

 Asn Met Asp Ser Ile Ala Ser Leu Val Met Ala Val Val Val Asn Glu
 130 135 140

 Glu Asp Gly Glu Gly Asp Ala Pro Asp Ala Thr Thr Gln Pro Gln Lys
 145 150 155 160

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Arg Lys Arg Leu Trp Gly Leu Val Val Cys His Asn Thr Thr Pro Arg
165 170 175

Phe Val Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Ala Gln Val
180 185 190

Phe Ala Ile His Val Asn Lys Glu Val Glu Leu Asp Asn Gln Met Val
195 200 205

Glu Lys
210

<210> 14
<211> 192
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:slr0473

<400> 14
His Met Ala Asn Ala Ala Leu Asn Arg Leu Arg Gln Gln Ala Asn Leu
1 5 10 15

Arg Asp Phe Tyr Asp Val Ile Val Glu Glu Val Arg Arg Met Thr Gly
20 25 30

Phe Asp Arg Val Met Leu Tyr Arg Phe Asp Glu Asn Asn His Gly Asp
35 40 45

Val Ile Ala Glu Asp Lys Arg Asp Asp Met Glu Pro Tyr Leu Gly Leu
50 55 60

His Tyr Pro Glu Ser Asp Ile Pro Gln Pro Ala Arg Arg Leu Phe Ile
65 70 75 80

His Asn Pro Ile Arg Val Ile Pro Asp Val Tyr Gly Val Ala Val Pro
85 90 95

Leu Thr Pro Ala Val Asn Pro Ser Thr Asn Arg Ala Val Asp Leu Thr
100 105 110

Glu Ser Ile Leu Arg Ser Ala Tyr His Cys His Leu Thr Tyr Leu Lys
115 120 125

Asn Met Gly Val Gly Ala Ser Leu Thr Ile Ser Leu Ile Lys Asp Gly
130 135 140

His Leu Trp Gly Leu Ile Ala Cys His His Gln Thr Pro Lys Val Ile
145 150 155 160

Pro Phe Glu Leu Arg Lys Ala Cys Glu Phe Phe Gly Arg Val Val Phe
165 170 175

Ser Asn Ile Ser Ala Gln Glu Asp Thr Glu Thr Phe Asp Tyr Arg Val
180 185 190

<210> 15
<211> 177
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:sl111473

<400> 15
a' cont.
Arg Phe Ile Asn Gln Ile Thr Gln His Ile Arg Gln Ser Leu Asn Leu
1 5 10 15

Glu Thr Val Leu Asn Thr Thr Val Ala Glu Val Lys Thr Leu Leu Gln
20 25 30

Val Asp Arg Val Leu Ile Tyr Arg Ile Trp Gln Asp Gly Thr Gly Ser
35 40 45

Ala Ile Thr Glu Ser Val Asn Ala Asn Tyr Pro Ser Ile Leu Gly Arg
50 55 60

Thr Phe Ser Asp Glu Val Phe Pro Val Glu Tyr His Gln Ala Tyr Thr
65 70 75 80

Lys Gly Lys Val Arg Ala Ile Asn Asp Ile Asp Gln Asp Asp Ile Glu
85 90 95

Ile Cys Leu Ala Asp Phe Val Lys Gln Phe Gly Val Lys Ser Lys Leu
100 105 110

Val Val Pro Ile Leu Gln His Asn Arg Ala Ser Ser Leu Asp Asn Glu
115 120 125

Ser Glu Phe Pro Tyr Leu Trp Gly Leu Leu Ile Thr His Gln Cys Ala

130 135 140

Phe Thr Arg Pro Trp Gln Pro Trp Glu Val Glu Leu Met Lys Gln Leu
 145 150 155 160

Ala Asn Gln Val Ala Ile Ala Ile Gln Gln Ser Glu Leu Tyr Glu Gln
 165 170 175

Leu

<210> 16
 <211> 173
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:Rcae

<400> 16
 Glu Leu Phe Ser Glu Val Thr Leu Lys Ile Arg Gln Ser Leu Gln Leu
 1 5 10 15

Lys Glu Ile Leu His Thr Thr Val Thr Glu Val Gln Arg Ile Leu Gln
 20 25 30

Ala Asp Arg Val Leu Ile Tyr His Val Leu Pro Asp Gly Thr Gly Lys
 35 40 45

Thr Ile Ser Glu Ser Val Leu Pro Asp Tyr Pro Thr Leu Met Asp Leu
 50 55 60

Glu Phe Pro Gln Glu Val Phe Pro Gln Glu Tyr Gln Gln Leu Tyr Ala
 65 70 75 80

Gln Gly Arg Val Arg Ala Ile Ala Asp Val His Asp Pro Thr Ala Gly
 85 90 95

Leu Ala Glu Cys Leu Val Glu Phe Val Asp Gln Phe His Ile Lys Ala
 100 105 110

Lys Leu Ile Val Pro Ile Val Gln Asn Leu Asn Ala Asn Ser Gln Asn
 115 120 125

Gln Leu Trp Gly Leu Leu Ile Ala His Gln Cys Asp Ser Val Arg Gln
 130 135 140

Trp Val Asp Phe Glu Leu Glu Leu Met Gln Gln Leu Ala Asp Gln Ile
145 150 155 160

Ser Ile Ala Leu Ser Gln Ala Gln Leu Leu Gly Arg Leu
165 170

<210> 17
<211> 168
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:slr1212

<400> 17
Ser Leu Leu Arg Glu Ile Thr Gln Arg Ile Arg Gln Ser Leu Asp Leu
1 5 10 15

Pro Thr Ile Phe Asn Thr Val Val Gln Glu Ile Arg Gln Phe Leu Glu
20 25 30

Ala Asp Arg Val Val Ile Phe Gln Phe Ser Pro Asp Ser Asp Phe Ser
35 40 45

Val Gly Asn Ile Val Ala Glu Ser Val Leu Ala Pro Phe Lys Pro Ile
50 55 60

Ile Asn Ser Ala Ile Glu Glu Thr Cys Phe Ser Asn Asn Tyr Ala Gln
65 70 75 80

Arg Tyr Gln Gln Gly Arg Ile Gln Val Ile Glu Asp Ile His Gln Ser
85 90 95

His Leu Arg Gln Cys His Ile Asp Phe Leu Ala Arg Leu Gln Val Arg
100 105 110

Ala Asn Leu Val Leu Pro Leu Ile Asn Asp Ala Ile Leu Trp Gly Leu
115 120 125

Leu Cys Ile His Gln Cys Asp Ser Ser Arg Val Trp Glu Gln Thr Glu
130 135 140

Ile Asp Leu Leu Lys Gln Ile Thr Asn Gln Phe Glu Ile Ala Ile Gln
145 150 155 160

Gln Ala Thr Leu Tyr Glu Gln Ala
165

<210> 18
<211> 165
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:sl110821b

<400> 18
Lys Leu Val Leu Lys Ile Ala Asn Lys Ile Arg Ala Ser Leu Asn Ile
1 5 10 15
Asn Asp Ile Leu Tyr Ser Thr Val Thr Glu Val Arg Gln Phe Leu Asn
20 25 30
Thr Asp Arg Val Val Leu Phe Lys Phe Asn Ser Gln Trp Ser Gly Gln
35 40 45
Val Val Thr Glu Ser His Asn Asp Phe Cys Arg Ser Ile Ile Asn Asp
50 55 60
Glu Ile Asp Asp Pro Cys Phe Lys Gly His Tyr Leu Arg Leu Tyr Arg
65 70 75 80
Glu Gly Arg Val Arg Ala Val Ser Asp Ile Glu Lys Ala Asp Leu Ala
85 90 95
Asp Cys His Lys Glu Leu Leu Arg His Tyr Gln Val Lys Ala Asn Leu
100 105 110
Val Val Pro Val Val Phe Asn Glu Asn Leu Trp Gly Leu Leu Ile Ala
115 120 125
His Glu Cys Lys Thr Pro Arg Tyr Trp Gln Glu Glu Asp Leu Gln Leu
130 135 140
Leu Met Glu Leu Ala Thr Gln Val Ala Ile Ala Ile His Gln Gly Glu
145 150 155 160
Leu Tyr Glu Gln Leu
165

<210> 19
<211> 165
<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism:sl111124

<400> 19

Lys Leu Leu Ser Ser Ile Ser Gln Arg Ile Arg Glu Ser Leu Lys Leu
1 5 10 15

Glu Thr Ile Leu Arg Thr Thr Val Thr Glu Val Arg Arg Thr Ile His
20 25 30

Ala Asp Arg Val Leu Ile His His Ile Gln Glu Asp Gly Leu Gly Thr
35 40 45

Thr Ile Ala Glu Ser Val Val Asn Gly Gln Pro Ser Val Met Gln Met
50 55 60

Asp Leu Ser Pro Glu Ser Phe Pro Pro Glu Cys Tyr Gln Arg Tyr Leu
65 70 75 80

Asn Gly Tyr Ile Tyr Ala Ser Arg Asp Gln Leu Pro Asp Cys Ala Ile
85 90 95

Asn Cys Ala Val Gln Cys Phe Thr Val Ala Glu Ser Gln Ser Arg Ile
100 105 110

Val Ala Pro Ile Val Phe Asp His Ser Leu Trp Gly Leu Leu Ile Val
115 120 125

His Gln Cys Ser Ser Ser Arg Thr Trp Gln Thr Ala Glu Ile Gln Leu
130 135 140

Met Gln Ser Leu Gly Asn Gln Leu Ala Ile Ala Ile Gln Gln Ser Leu
145 150 155 160

Leu Tyr Glu Arg Leu
165

<210> 20

<211> 165

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism:sl110041

<400> 20

Gln Ile Leu Lys Glu Leu Thr Leu Lys Ile Ser Ala Ala Ile Asn Ser
1 5 10 15

Glu Gln Val Phe Asp Ile Ala Ala Gln Glu Ile Arg Leu Ala Leu Lys
20 25 30

Ala Asp Arg Val Ile Val Tyr Arg Phe Asp Ala Thr Trp Ala Gly Thr
35 40 45

Val Ile Val Glu Ser Val Ala Glu Gly Tyr Pro Lys Ala Leu Gly Ala
50 55 60

Thr Ile Ala Asp Pro Cys Phe Ala Asp Ser Tyr Val Glu Lys Tyr Arg
65 70 75 80

Ser Gly Arg Ile Gln Ala Thr Arg Asp Ile Tyr Asn Ala Gly Leu Thr
85 90 95

Pro Cys His Ile Gly Gln Leu Lys Pro Phe Glu Val Lys Ala Asn Leu
100 105 110

Val Ala Pro Ile Asn Tyr Lys Gly Asn Leu Leu Gly Leu Leu Ile Ala
115 120 125

His Gln Cys Ser Gly Pro Arg Asp Trp His Gln Asn Glu Ile Asp Leu
130 135 140

Phe Gly Gln Leu Thr Val Gln Val Gly Leu Ala Leu Glu Arg Ser Asp
145 150 155 160

Leu Leu Ala Gln Gln
165

<210> 21

<211> 170

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism:slr1393

<400> 21

Arg Ala Leu Thr Arg Val Ile Glu Gly Ile Arg Gln Thr Leu Glu Leu
1 5 10 15

Gln Asn Ile Phe Arg Ala Thr Ser Asp Glu Val Arg His Leu Leu Ser

20 25 30
 Cys Asp Arg Val Leu Val Tyr Arg Phe Asn Pro Asp Trp Ser Gly Glu
 35 40 45
 Phe Ile His Glu Ser Val Ala Gln Met Trp Glu Pro Leu Lys Asp Leu
 50 55 60
 Gln Asn Asn Phe Pro Leu Trp Gln Asp Thr Tyr Leu Gln Glu Asn Glu
 65 70 75 80
 Gly Gly Arg Tyr Arg Asn His Glu Ser Leu Ala Val Gly Asp Val Glu
 85 90 95
 Thr Ala Gly Phe Thr Asp Cys His Leu Asp Asn Leu Arg Arg Phe Glu
 100 105 110
 Ile Arg Ala Phe Leu Thr Val Pro Val Phe Val Gly Glu Gln Leu Trp
 115 120 125
 Gly Leu Leu Gly Ala Tyr Gln Asn Gly Ala Pro Arg His Trp Gln Ala
 130 135 140
 Arg Glu Ile His Leu Leu His Gln Ile Ala Asn Gln Leu Gly Val Ala
 145 150 155 160
 Val Tyr Gln Ala Gln Leu Leu Ala Arg Phe
 165 170

<210> 22
 <211> 188
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:sl111969

<400> 22
 Lys Leu Leu Ser Gln Val Ile Ala Gln Ile Arg Gln Ser Leu Asp Leu
 1 5 10 15
 Ser Glu Ile Leu Asn Asn Ala Val Thr Ala Val Gln Lys Phe Leu Phe
 20 25 30
 Val Asp Arg Leu Val Ile Tyr Gln Phe His Tyr Ser Gln Pro Ser Leu
 35 40 45

Thr Pro Leu Glu Glu Asn Gln Ile Pro Ala Pro Arg Pro Arg Gln Gln
50 55 60

Tyr Gly Glu Val Thr Tyr Glu Ala Arg Arg Ser Pro Glu Ile Asp Thr
65 70 75 80

Met Leu Gly Ile Met Thr Glu Asn Asp Cys Phe Ser Gln Val Phe Ser
85 90 95

Tyr Glu Gln Lys Tyr Leu Lys Gly Ala Val Val Ala Val Ser Asp Ile
100 105 110

Glu Asn His Tyr Ser Ser Ser Tyr Cys Leu Val Gly Leu Leu Gln Arg
115 120 125

Tyr Gln Val Arg Ala Lys Leu Val Ala Pro Ile Ile Val Glu Gly Gln
130 135 140

Leu Trp Gly Leu Leu Ile Ala His Gln Cys His His Pro Arg Gln Trp
145 150 155 160

Leu Asp Ser Glu Lys Asn Phe Leu Gly Gln Ile Gly Glu His Leu Ala
165 170 175

Val Ala Ile Val Gln Ser Leu Leu Tyr Ser Glu Val
180 185

<210> 23
<211> 187
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:sl110821a

<400> 23
Asp Phe Leu Arg Asn Val Ile Asn Lys Phe His Arg Ala Leu Thr Leu
1 5 10 15

Arg Glu Thr Leu Gln Val Ile Val Glu Glu Ala Arg Ile Phe Leu Gly
20 25 30

Val Asp Arg Val Lys Ile Tyr Lys Phe Ala Ser Asp Gly Ser Gly Glu
35 40 45

Val Leu Ala Glu Ala Val Asn Arg Ala Ala Leu Pro Ser Leu Leu Gly
50 55 60

Leu His Phe Pro Val Glu Asp Ile Pro Pro Gln Ala Arg Glu Glu Leu
65 70 75 80

Gly Asn Gln Arg Lys Met Ile Ala Val Asp Val Ala His Arg Arg Lys
85 90 95

Lys Ser His Glu Leu Ser Gly Arg Ile Ser Pro Thr Glu His Ser Asn
100 105 110

Gly His Tyr Thr Thr Val Asp Ser Cys His Ile Gln Tyr Leu Leu Ala
115 120 125

Met Gly Val Leu Ser Ser Leu Thr Val Pro Val Met Gln Asp Gln Gln
130 135 140

Leu Trp Gly Ile Met Ala Val His His Ser Lys Pro Arg Arg Phe Thr
145 150 155 160

Glu Gln Glu Trp Glu Thr Met Ala Leu Leu Ser Lys Glu Val Ser Leu
165 170 175

Ala Ile Thr Gln Ser Gln Leu Ser Arg Gln Val
180 185

<210> 24
<211> 210
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Cph2-N197

<220>
<221> DOMAIN
<222> (201)..(210)
<223> Strep-tag

<400> 24
Met Asn Pro Asn Arg Ser Leu Glu Asp Phe Leu Arg Asn Val Ile Asn
1 5 10 15

Lys Phe His Arg Ala Leu Thr Leu Arg Glu Thr Leu Gln Val Ile Val
20 25 30

Glu Glu Ala Arg Ile Phe Leu Gly Val Asp Arg Val Lys Ile Tyr Lys
35 40 45

Phe Ala Ser Asp Gly Ser Gly Glu Val Leu Ala Glu Ala Val Asn Arg
50 55 60

Ala Ala Leu Pro Ser Leu Gly Leu His Phe Pro Val Glu Asp Ile Pro
65 70 75 80

Pro Gln Ala Arg Glu Glu Leu Gly Asn Gln Arg Lys Met Ile Ala Val
85 90 95

Asp Val Ala His Arg Arg Lys Lys Ser His Glu Leu Ser Gly Arg Ile
100 105 110

Ser Pro Thr Glu His Ser Asn Gly His Tyr Thr Thr Val Asp Ser Cys
115 120 125

His Ile Gln Tyr Leu Leu Ala Met Gly Val Leu Ser Leu Thr Val Pro
130 135 140

Val Met Gln Asp Gln Gln Leu Trp Gly Ile Met Ala Val His His Ser
145 150 155 160

Lys Pro Arg Arg Phe Thr Glu Gln Glu Trp Glu Thr Met Ala Leu Leu
165 170 175

Ser Lys Glu Val Ser Leu Ala Ile Thr Gln Ser Gln Leu Ser Arg Gln
180 185 190

Val His Gln Gly Arg Pro Ala Gly Ser Ala Trp Arg His Pro Gln Phe
195 200 205

Gly Gly
210

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